

RAW SEQUENCE LISTING

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Application Serial Number: 10/527,707

Source: PCT

Date Processed by STIC: 4-19-06

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PCT

RAW SEQUENCE LISTING

DATE: 04/19/2006

PATENT APPLICATION: US/10/527,707

TIME: 12:33:15

Input Set : A:\41065.txt

Output Set: N:\CRF4\04192006\J527707.raw

3 <110> APPLICANT: Acharya,, et al.

5 <120> TITLE OF INVENTION: Crystal Structure of an Angiotensin-Converting Enzyme (ACE)

and

6 Uses Thereof

8 <130> FILE REFERENCE: 30699/41065

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/527,707

C--> 10 <141> CURRENT FILING DATE: 2005-03-11

10 <160> NUMBER OF SEQ ID NOS: 11

12 <170> SOFTWARE: PatentIn version 3.3

14 <210> SEQ ID NO: 1

15 <211> LENGTH: 701

16 <212> TYPE: PRT

17 <213> ORGANISM: Homo sapiens

19 <400> SEQUENCE: 1

21 Ser Gln Gln Val Thr Val Thr His Gly Thr Ser Ser Gln Ala Thr Thr

22 1 5 10 15

25 Ser Ser Gln Thr Thr Thr His Gln Ala Thr Ala His Gln Thr Ser Ala

26 20 25 30

29 Gln Ser Pro Asn Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val

30 35 40 45

33 Glu Glu Tyr Asp Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu

34 50 55 60

37 Ala Asn Trp Asn Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile

38 65 70 75 80

41 Leu Leu Gln Lys Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly

42 85 90 95

45 Thr Gln Ala Arg Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile

46 100 105 110

49 Lys Arg Ile Ile Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro

50 115 120 125

53 Ala Gln Glu Leu Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr

54 130 135 140

57 Thr Tyr Ser Val Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln

58 145 150 155 160

61 Leu Glu Pro Asp Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu

62 165 170 175

65 Asp Leu Leu Trp Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala

66 180 185 190

69 Ile Leu Gln Phe Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala

70 195 200 205

73 Arg Leu Asn Gly Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr

74 210 215 220

77 Glu Thr Pro Ser Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu

78 225 230 235 240

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81 Gln Pro Leu Tyr Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His
82                245                        250                        255
85 Arg His Tyr Gly Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala
86                260                        265                        270
89 His Leu Leu Gly Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp
90                275                        280                        285
93 Leu Val Val Pro Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala
94                290                        295                        300
97 Met Leu Lys Gln Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp
98 305                310                        315                        320
101 Asp Phe Phe Thr Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp
102                325                        330                        335
105 Asn Lys Ser Met Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys
106                340                        345                        350
109 His Ala Ser Ala Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys
110                355                        360                        365
113 Gln Cys Thr Thr Val Asn Leu Glu Asp Leu Val Val Ala His His Glu
114                370                        375                        380
117 Met Gly His Ile Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala
118 385                390                        395                        400
121 Leu Arg Glu Gly Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val
122                405                        410                        415
125 Leu Ala Leu Ser Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu
126                420                        425                        430
129 Leu Ser Ser Glu Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met
130                435                        440                        445
133 Lys Met Ala Leu Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val
134                450                        455                        460
137 Asp Gln Trp Arg Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn
138 465                470                        475                        480
141 Tyr Asn Gln Glu Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys
142                485                        490                        495
145 Pro Pro Val Pro Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe
146                500                        505                        510
149 His Ile Pro Ser Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile
150                515                        520                        525
153 Ile Gln Phe Gln Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr
154                530                        535                        540
157 Gly Pro Leu His Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln
158 545                550                        555                        560
161 Arg Leu Ala Thr Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu
162                565                        570                        575
165 Ala Met Gln Leu Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met
166                580                        585                        590
169 Leu Ser Tyr Phe Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu
170                595                        600                        605
173 Leu His Gly Glu Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn
174                610                        615                        620
177 Ser Ala Arg Ser Glu Gly Pro Leu Pro Asp Ser Gly Arg Val Ser Phe

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178 625          630          635          640
181 Leu Gly Leu Asp Leu Asp Ala Gln Gln Ala Arg Val Gly Gln Trp Leu
182          645          650          655
185 Leu Leu Phe Leu Gly Ile Ala Leu Leu Val Ala Thr Leu Gly Leu Ser
186          660          665          670
189 Gln Arg Leu Phe Ser Ile Arg His Arg Ser Leu His Arg His Ser His
190          675          680          685
193 Gly Pro Gln Phe Gly Ser Glu Val Glu Leu Arg His Ser
194          690          695          700
197 <210> SEQ ID NO: 2
198 <211> LENGTH: 589
199 <212> TYPE: PRT
200 <213> ORGANISM: Homo sapiens
202 <400> SEQUENCE: 2
204 Leu Val Thr Asp Glu Ala Glu Ala Ser Lys Phe Val Glu Glu Tyr Asp
205 1          5          10          15
208 Arg Thr Ser Gln Val Val Trp Asn Glu Tyr Ala Glu Ala Asn Trp Asn
209          20          25          30
212 Tyr Asn Thr Asn Ile Thr Thr Glu Thr Ser Lys Ile Leu Leu Gln Lys
213          35          40          45
216 Asn Met Gln Ile Ala Asn His Thr Leu Lys Tyr Gly Thr Gln Ala Arg
217          50          55          60
220 Lys Phe Asp Val Asn Gln Leu Gln Asn Thr Thr Ile Lys Arg Ile Ile
221 65          70          75          80
224 Lys Lys Val Gln Asp Leu Glu Arg Ala Ala Leu Pro Ala Gln Glu Leu
225          85          90          95
228 Glu Glu Tyr Asn Lys Ile Leu Leu Asp Met Glu Thr Thr Tyr Ser Val
229          100          105          110
232 Ala Thr Val Cys His Pro Asn Gly Ser Cys Leu Gln Leu Glu Pro Asp
233          115          120          125
236 Leu Thr Asn Val Met Ala Thr Ser Arg Lys Tyr Glu Asp Leu Leu Trp
237          130          135          140
240 Ala Trp Glu Gly Trp Arg Asp Lys Ala Gly Arg Ala Ile Leu Gln Phe
241 145          150          155          160
244 Tyr Pro Lys Tyr Val Glu Leu Ile Asn Gln Ala Ala Arg Leu Asn Gly
245          165          170          175
248 Tyr Val Asp Ala Gly Asp Ser Trp Arg Ser Met Tyr Glu Thr Pro Ser
249          180          185          190
252 Leu Glu Gln Asp Leu Glu Arg Leu Phe Gln Glu Leu Gln Pro Leu Tyr
253          195          200          205
256 Leu Asn Leu His Ala Tyr Val Arg Arg Ala Leu His Arg His Tyr Gly
257          210          215          220
260 Ala Gln His Ile Asn Leu Glu Gly Pro Ile Pro Ala His Leu Leu Gly
261 225          230          235          240
264 Asn Met Trp Ala Gln Thr Trp Ser Asn Ile Tyr Asp Leu Val Val Pro
265          245          250          255
268 Phe Pro Ser Ala Pro Ser Met Asp Thr Thr Glu Ala Met Leu Lys Gln
269          260          265          270
272 Gly Trp Thr Pro Arg Arg Met Phe Lys Glu Ala Asp Asp Phe Phe Thr

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273          275          280          285
276 Ser Leu Gly Leu Leu Pro Val Pro Pro Glu Phe Trp Asn Lys Ser Met
277          290          295          300
280 Leu Glu Lys Pro Thr Asp Gly Arg Glu Val Val Cys His Ala Ser Ala
281 305          310          315          320
284 Trp Asp Phe Tyr Asn Gly Lys Asp Phe Arg Ile Lys Gln Cys Thr Thr
285          325          330          335
288 Val Asn Leu Glu Asp Leu Val Val Ala His His Glu Met Gly His Ile
289          340          345          350
292 Gln Tyr Phe Met Gln Tyr Lys Asp Leu Pro Val Ala Leu Arg Glu Gly
293          355          360          365
296 Ala Asn Pro Gly Phe His Glu Ala Ile Gly Asp Val Leu Ala Leu Ser
297          370          375          380
300 Val Ser Thr Pro Lys His Leu His Ser Leu Asn Leu Leu Ser Ser Glu
301 385          390          395          400
304 Gly Gly Ser Asp Glu His Asp Ile Asn Phe Leu Met Lys Met Ala Leu
305          405          410          415
308 Asp Lys Ile Ala Phe Ile Pro Phe Ser Tyr Leu Val Asp Gln Trp Arg
309          420          425          430
312 Trp Arg Val Phe Asp Gly Ser Ile Thr Lys Glu Asn Tyr Asn Gln Glu
313          435          440          445
316 Trp Trp Ser Leu Arg Leu Lys Tyr Gln Gly Leu Cys Pro Pro Val Pro
317          450          455          460
320 Arg Thr Gln Gly Asp Phe Asp Pro Gly Ala Lys Phe His Ile Pro Ser
321 465          470          475          480
324 Ser Val Pro Tyr Ile Arg Tyr Phe Val Ser Phe Ile Ile Gln Phe Gln
325          485          490          495
328 Phe His Glu Ala Leu Cys Gln Ala Ala Gly His Thr Gly Pro Leu His
329          500          505          510
332 Lys Cys Asp Ile Tyr Gln Ser Lys Glu Ala Gly Gln Arg Leu Ala Thr
333          515          520          525
336 Ala Met Lys Leu Gly Phe Ser Arg Pro Trp Pro Glu Ala Met Gln Leu
337          530          535          540
340 Ile Thr Gly Gln Pro Asn Met Ser Ala Ser Ala Met Leu Ser Tyr Phe
341 545          550          555          560
344 Lys Pro Leu Leu Asp Trp Leu Arg Thr Glu Asn Glu Leu His Gly Glu
345          565          570          575
348 Lys Leu Gly Trp Pro Gln Tyr Asn Trp Thr Pro Asn Ser
349          580          585
352 <210> SEQ ID NO: 3
353 <211> LENGTH: 39
354 <212> TYPE: DNA
355 <213> ORGANISM: Artificial sequence
357 <220> FEATURE:
358 <223> OTHER INFORMATION: Synthetic primer
360 <400> SEQUENCE: 3
361 gaggccaatt ggaactacaa cacccagatc accacagag
364 <210> SEQ ID NO: 4
365 <211> LENGTH: 36

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366 <212> TYPE: DNA
367 <213> ORGANISM: Artificial sequence
369 <220> FEATURE:
370 <223> OTHER INFORMATION: Synthetic primer
372 <400> SEQUENCE: 4
373 atgcaaataag cccagcacac ccttaagtac ggcacc          36
376 <210> SEQ ID NO: 5
377 <211> LENGTH: 40
378 <212> TYPE: DNA
379 <213> ORGANISM: Artificial sequence
381 <220> FEATURE:
382 <223> OTHER INFORMATION: Synthetic primer
384 <400> SEQUENCE: 5
385 gaagtttgat gttaaccagt tgcagcagac cactatcaag      40
388 <210> SEQ ID NO: 6
389 <211> LENGTH: 30
390 <212> TYPE: DNA
391 <213> ORGANISM: Artificial sequence
393 <220> FEATURE:
394 <223> OTHER INFORMATION: Synthetic primer
396 <400> SEQUENCE: 6
397 gtgtgccacc cgcaaggtag ctgcctgcag          30
400 <210> SEQ ID NO: 7
401 <211> LENGTH: 36
402 <212> TYPE: DNA
403 <213> ORGANISM: Artificial sequence
405 <220> FEATURE:
406 <223> OTHER INFORMATION: Synthetic primer
408 <400> SEQUENCE: 7
409 ccgtgcctcc tgaattctgg cagaagtoga tgctgg          36
412 <210> SEQ ID NO: 8
413 <211> LENGTH: 30
414 <212> TYPE: DNA
415 <213> ORGANISM: Artificial sequence
417 <220> FEATURE:
418 <223> OTHER INFORMATION: Synthetic primer
420 <400> SEQUENCE: 8
421 acgggccagc cccagatgag cgcttcggcc          30
424 <210> SEQ ID NO: 9
425 <211> LENGTH: 40
426 <212> TYPE: DNA
427 <213> ORGANISM: Artificial sequence
429 <220> FEATURE:
430 <223> OTHER INFORMATION: Synthetic primer
432 <400> SEQUENCE: 9
433 ctctgtggtg atctgggtgt tgtagttcca attggcctcg      40
436 <210> SEQ ID NO: 10
437 <211> LENGTH: 36
438 <212> TYPE: DNA

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VERIFICATION SUMMARY

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Input Set : A:\41065.txt

Output Set: N:\CRF4\04192006\J527707.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date